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AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of claims in the application:

Listing of Claims:

Claims 1-101 (cancelled)

102. (Currently Amended) A method for analyzing a polynucleotide, comprising:

a) providing a polynucleotide having homology to a defined DNA sequence;

b) calculating the masses of two or more polypeptides encoded in two or more ~~overlapping~~ different reading frames of said defined DNA sequence thereby obtaining a set of predicted mass values;

c) expressing two or more polypeptides from two or more ~~overlapping~~ different reading frames of said polynucleotide, thereby creating two or more expressed polypeptides;

d) measuring the masses of said two or more expressed polypeptides, thereby obtaining a set of observed mass values; and

e) comparing said set of predicted mass values to said set of observed mass values.

103. (Previously Presented) The method of claim 102, wherein the polynucleotide contains a difference with respect to the defined DNA sequence and wherein said difference is selected from the group consisting of single nucleotide polymorphism, single nucleotide substitution, single nucleotide deletion, single nucleotide insertion, multiple nucleotide substitution, multiple nucleotide deletion, multiple nucleotide insertion, DNA duplication, DNA inversion, DNA translocation, and DNA deletion/substitution.

104. (Previously Presented) The method of claim 102, wherein the polynucleotide comprises an exon.

105. (Previously Presented) The method of claim 102, wherein the polynucleotide comprises a cDNA.

106. (Previously Presented) The method of claim 102, wherein the polynucleotide comprises at least one predetermined epitope tag.

107. (Previously Presented) The method of claim 102, wherein the expressed polypeptides are expressed in a living cell.

108. (Previously Presented) The method of claim 102, wherein the expressed polypeptides are expressed in a cell free system.

109. (Previously Presented) The method of claim 108, wherein said cell free system is selected from the group consisting of E. coli extract, rabbit reticulocyte extract, and wheat germ extract.

110. (Previously Presented) The method of claim 102, further comprising purification of the polypeptides prior to measuring their masses.

111. (Previously Presented) The method of claim 110, wherein said purification comprises a method selected from the group consisting of gel electrophoresis, capillary electrophoresis, liquid chromatography (LC), capillary liquid chromatography, high performance liquid chromatography (HPLC), differential centrifugation, filtration, gel filtration, membrane chromatography, affinity purification, biomolecular interaction analysis (BIA), ligand affinity purification, glutathione-S-transferase affinity chromatography, cellulose binding protein affinity chromatography, maltose binding protein affinity chromatography, avidin/streptavidin affinity chromatography, S-tag affinity chromatography, thioredoxin affinity chromatography, metal-chelate affinity chromatography, immobilized metal affinity chromatography, epitope-tag affinity chromatography,

immunoaffinity chromatography, immunoaffinity capture, capture using bioreactive mass spectrometer probes, mass spectrometric immunoassay, and immunoprecipitation.

112. (Previously Presented) The method of claim 102 wherein the polypeptide masses are measured by a method selected from the group consisting of mass spectrometry, MALDI-TOF mass spectrometry, electrospray ionization mass spectrometry (ESI), tandem mass spectrometry (MS/MS), quadripole time of flight spectrometry (Q-TOF), Fourier transform ion cyclotron resonance (FTICR) mass spectrometry, gel electrophoresis, capillary electrophoresis, and high performance liquid chromatography (HPLC).